

Please delete the title, page 1, line 1, and replace it with the following:

--POLYNUCLEOTIDE ENCODING IL-1 ZETA POLYPEPTIDE--

Please delete the paragraphs at page 4, lines 1 through 27, and replace them with the following:

--In addition, when a peptide fingerprint of an unknown protein is obtained, it can be compared to a database of known proteins to assist in the identification of the unknown protein using mass spectrometry (W.J. Henzel et al., *Proc. Natl. Acad. Sci. USA* 90:5011-5015, 1993; D. Fenyo et al., *Electrophoresis* 19:998-1005, 1998). A variety of computer software programs to facilitate these comparisons are accessible via the Internet, such as Protein Prospector (on the World Wide Web [www], at uscf.edu, search the site for prospector), MultiIdent (on the World Wide Web [www], at expasy.org, search for MultiIdent), PeptideSearch (on the World Wide Web [www], at mann.embl-heidelberg.de, using the PeptideSearch link), and ProFound (as described by Zhang and Chait, *Anal. Chem.* 72:2482, 2000, available online from Rockefeller University by performing a web search on 'profound' and 'rockefeller'). These programs allow the user to specify the cleavage agent and the molecular weights of the fragmented peptides within a designated tolerance. The programs compare these molecular weights to protein molecular weight information stored in databases to assist in determining the identity of the unknown protein. Accurate information concerning the number of fragmented peptides and the precise molecular weight of those peptides is required for accurate identification. Therefore, increasing the accuracy in determining the number of fragmented peptides and their molecular weight should result in enhanced likelihood of success in the identification of unknown proteins.

In addition, peptide digests of unknown proteins can be sequenced using tandem mass spectrometry (MS/MS) and the resulting sequence searched against databases (J.K. Eng, et al., *J. Am. Soc. Mass Spec.* 5:976-989 (1994); M. Mann and M. Wilm, *Anal. Chem.* 66:4390-4399 (1994); J.A. Taylor and R.S. Johnson, *Rapid Comm. Mass Spec.* 11:1067-1075 (1997)). Searching programs that can be used in this process exist on the Internet, such as Lutfisk 97(on the World Wide Web, at i-mass.com), and the Protein Prospector, Peptide Search and ProFound programs described above. Therefore, adding the sequence of a gene and its predicted protein sequence and peptide fragments to a sequence database can aid in the identification of unknown proteins using tandem mass spectrometry.--